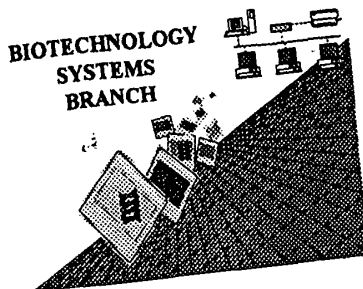


# RAW SEQUENCE LISTING ERROR REPORT



0590  
1212

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/992,600  
Source: OIP  
Date Processed by STIC: 12/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
  - 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
- FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

## **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/992,600

DATE: 12/05/2001

TIME: 12:20:09

Input Set : D:\Seqlist.txt

Output Set: N:\CRF3\11212001\I992600.raw

*nr 2-3*

Does Not Comply  
Corrected Diskette Needed

OK> 3 <110> APPLICANT: Benjanin, Stephane  
 4 Tanaka, Hiroaki  
 6 <120> TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
 8 <130> FILE REFERENCE: 91.US4.DIV  
 10 <140> CURRENT APPLICATION NUMBER: US/09/992,600  
 11 <141> CURRENT FILING DATE: 2001-11-13  
 13 <150> PRIOR APPLICATION NUMBER: US 09/924,340  
 14 <151> PRIOR FILING DATE: 2001-08-06  
 16 <150> PRIOR APPLICATION NUMBER: PCT/IB01/01715  
 17 <151> PRIOR FILING DATE: 2001-08-06  
 19 <150> PRIOR APPLICATION NUMBER: US 60/305,456  
 20 <151> PRIOR FILING DATE: 2001-07-13  
 22 <150> PRIOR APPLICATION NUMBER: US 60/302,277  
 23 <151> PRIOR FILING DATE: 2001-06-29  
 25 <150> PRIOR APPLICATION NUMBER: US 60/298,698  
 26 <151> PRIOR FILING DATE: 2001-06-15  
 28 <150> PRIOR APPLICATION NUMBER: US 60/293,574  
 29 <151> PRIOR FILING DATE: 2001-05-25  
 31 <160> NUMBER OF SEQ ID NOS: 112  
 33 <170> SOFTWARE: JPatent

## ERRORED SEQUENCES

6602 <210> SEQ ID NO: 112  
 6603 <211> LENGTH: 387  
 6604 <212> TYPE: PRT  
 6605 <213> ORGANISM: Homo sapiens  
 6607 <400> SEQUENCE: 112

*P. 2*

6608	Met	Ser	Thr	Phe	Phe	Ser	Asp	Thr	Ala	Trp	Ile	Cys	Leu	Ala	Val	Pro
6609	1				5					10					15	
6610	Thr	Val	Leu	Cys	Gly	Thr	Val	Phe	Cys	Lys	Tyr	Lys	Lys	Ser	Ser	Gly
6611				20					25					30		
6612	Gln	Leu	Trp	Ser	Trp	Met	Val	Cys	Leu	Ala	Gly	Leu	Cys	Ala	Val	Cys
6613				35				40					45			
6614	Leu	Leu	Ile	Leu	Ser	Pro	Phe	Trp	Gly	Leu	Ile	Leu	Phe	Ser	Val	Ser
6615		50					55					60				
6616	Cys	Phe	Leu	Met	Tyr	Thr	Tyr	Leu	Ser	Gly	Gln	Glu	Leu	Leu	Pro	Val
6617	65					70					75				80	
6618	Asp	Gln	Lys	Ala	Val	Leu	Val	Thr	Gly	Gly	Asp	Cys	Gly	Leu	Gly	His
6619				85					90					95		
6620	Ala	Leu	Cys	Lys	Tyr	Leu	Asp	Glu	Leu	Gly	Phe	Thr	Val	Phe	Ala	Gly
6621				100					105					110		
6622	Val	Leu	Asn	Glu	Asn	Gly	Pro	Gly	Ala	Glu	Glu	Leu	Arg	Arg	Thr	Cys
6623			115					120					125			
6624	Ser	Pro	Arg	Leu	Ser	Val	Leu	Gln	Met	Asp	Ile	Thr	Lys	Pro	Val	Gln
6625		130					135					140				

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/992,600

DATE: 12/05/2001

TIME: 12:20:11

Input Set : D:\Seqlist.txt

Output Set: N:\CRF3\11212001\I992600.raw

```

6626 Ile Lys Asp Ala Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly
6627 145 150 155 160
6628 Leu Trp Ala Val Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp
6629 165 170 175
6630 Gly Glu Leu Leu Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn
6631 180 185 190
6632 Phe Phe Gly Thr Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg
6633 195 200 205
6634 Lys Ser Lys Gly Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala
6635 210 215 220
6636 Pro Val Glu Arg Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr
6637 225 230 235 240
6638 Met Phe Ser Ser Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys
6639 245 250 255
6640 Val Ala Ser Ile Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr
6641 260 265 270
6642 Ser Asp Lys Trp Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro
6643 275 280 285
6644 Ala Glu Val Gln Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg
6645 290 295 300
6646 Asn Phe Leu Leu Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro
6647 305 310 315 320
6648 Val Leu Arg Asp Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala
6649 325 330 335
6650 Tyr Tyr Thr Pro Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His
6651 340 345 350
6652 Tyr Leu Pro Ile Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly
6653 355 360 365
6654 Gln Asp Lys Pro Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys
6655 370 375 380
6656 Lys Ala Pro
6657 385

```

E--&gt;

6658 (1) delete at end of file

*see next page for more errors*

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

*pyl*

<210> 30  
 <211> 258  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..20

<220>

<221> UNSURE

<222> (49) 29 ←

<223> Xaa = Glu, (\*)

<400> 30

Met Gly Arg Thr Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile  
 -20 -15 -10 -5  
 Gly Ala Gly Ala Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp  
 1 5 10  
 Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser  
 15 20 25  
 (Xaa) Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala  
 30 35 40  
 Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val  
 45 50 55 60  
 Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser  
 65 70 75  
 Gly Ser His Ser Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe  
 80 85 90  
 Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg  
 95 100 105  
 Val Gly Thr Ile Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys  
 110 115 120  
 Pro Gly Gly Arg Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg  
 125 130 135 140  
 Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys  
 145 150 155  
 Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe  
 160 165 170  
 Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln  
 175 180 185  
 Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu  
 190 195 200  
 Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln  
 205 210 215 220  
 Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys  
 225 230 235  
 Lys Lys

the Xaa is at location 29 (a positive (+) 29)  
 Xaa cannot represent a stop codon  
 or a gap in the sequence

"49" denotes  
 a positive (+)  
 49, not the  
 49<sup>th</sup> position  
 in the  
 sequence,  
 when the  
 sequence includes  
 negative  
 numbers

e.g. if the  
 Xaa were in  
 the second position  
 in the sequence, the  
 <222>  
 Please <sup>sequence</sup> would be  
 correct an -19.  
 identical error  
 in Sequence 72.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/992,600

DATE: 12/05/2001

TIME: 12:20:12

Input Set : D:\Seqlist.txt

Output Set: N:\CRF3\11212001\I992600.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
 L:1477 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27  
 L:1477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
 L:1498 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27  
 L:1498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
 L:1544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
 L:1558 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
 L:1599 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:29  
 L:1599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29  
 L:1662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
 L:4096 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:71  
 L:4096 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71  
 L:4163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72  
 L:6658 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:112